In the Specification:

Please replace the Title as follows:

~~High Throughput Mutagenesis Screening Method~~

Mutant *Pseudomonas mendocina* Cutinase

On page 7, please amend the paragraph at lines 7-14 as follows:

Following selection of the subset of amino acid positions in the protein for mutagenesis (step 2 in Fig. 2), site-saturation libraries are made at the selected sites by random substitutions of all 19 amino acids using conventional oligonucleotide-directed mutagenesis (step 4 in Fig. 1). Such conventional library formation is well known to those skilled in the art and was carried out generally as described by Airaksinen, A and Hovi, T. (1998) Nucleic Acids Research, Vol. 26, No. 2: 576-581. Other site-saturation methods may be used and kits, such as the Stratagene ~~Quik-Change~~™ QUIK-CHANGE® kit or the Sculptor Mutagenesis Kit (Amersham, UK) will be apparent to those skilled in the art.

On page 10, please amend the paragraph at lines 14-25 as follows:

Site-saturation variant libraries were created at amino acid positions corresponding to residue positions 57-66, 68, 85 ,86, 88, 125-127, 130, 148-152, 154,155, 176-183, and 204-211 of SEQ ID NO:2 in *P. mendocina* cutinase, expressed in *Bacillus subtilis* strain 3934. The sequence of the parent cutinase is attached hereto as Fig. 17. Libraries were created with the Stratagene ~~Quik-Change~~™ QUIK-CHANGE® kit using oligonucleotide primers randomized with NN(G/C) at the target position. Each selected amino acid was randomly replaced with all 19 possible alternatives. Colonies obtained from the variant libraries were selected and placed into 96-well growth plates that contained 100 µL/well of MOPS 1A starter medium. The plates were incubated at 37°C overnight with continuous humidified shaking at 260 rpm. A sample from each well was replicated into a Millipore 96-well filter plate which contained 200 µL/well of MOPS-Urea medium. 50 µL of 45% glycerol was added to each well of the initial growth plates, which then were stored at -70°C.

On page 13, please amend the paragraph at lines 20-32 as follows:

The results from the TCA assay, the PET hydrolysis assay, and the stability assay were calculated, using conventional, known formulas as set out above, using ~~Excel™~~ EXCEL® spreadsheet software. Variants were graded and ranked for stability and hydrolysis activity. Table 1 shows the results obtained from the site-saturation mutagenesis procedure described in this example. The results were graded and ~~color~~ coded as follows: ~~green~~ (▒▒▒)=more than 2% of the variants at the listed sites had significantly greater activity than the control (beneficial mutation); ~~blue~~ (▒▒▒) =the majority of the variants had unchanged activity (neutral mutation); ~~red~~ (▒▒▒) =the majority of the variants had significantly decreased activity relative to the control (detrimental mutation) ; and ~~brown~~ (▒▒▒) =approximately half of the variants had unchanged activity and half had decreased activity (neutral mutation). The ~~color~~ coding was repeated using the same ~~colors~~ shading and same percentage criteria for stability results. As can be seen in Table 1, ~~color~~ coding easily identifies those variants having both desired enzyme properties.

On pages 13-14, please amend the legend to Table 1 as follows:

Table 1 shows the results obtained from a typical enzyme system. The results are ~~color~~-coded as follows: ~~Green~~ (▒▒▒)--more than 2% of the clones had significantly greater activity than control. ~~Blue~~ (▒▒▒) – the majority were unchanged. ~~Red~~ (▒▒▒) – the majority had significantly decreased activity relative to the control. ~~Brown~~ (▒▒▒) – approximately half were unchanged and half were decreased.